

## SEQUENCE LISTING

**TECH CENTER 1600/2900** 

Chmura, Albert The Regents of the University of California <120> Engineering Antibodies That Bind Irreversibly <130> 023070-099120US <140> US 09/671,953 <141> 2000-09-27 <150> US 60/156,194 <151> 1999-09-27 <150> US 60/208,684 <151> 2000-05-31 <160> 23 <170> PatentIn Ver. 2.1 <210> 1 <211> 753 <212> DNA <213> Artificial Sequence

<223> Description of Artificial Sequence:nucleic acid that encodes Fab heavy chain of CHA255

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<210> 2 <211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:nucleic acid that encodes light chain mutant with Cys substituted for Asn at position 97 of CHA255

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qaaaaaccaq atcatttatt cactgqtcta ataggtggta ccaataaccg ggctccgggt 180
gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
qcacaqactq aaqatqagqc aagatatttc tgtgctctat ggtactcctg cctctgggtr 300
ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcaccetga egetgageaa agcagactae gagaaacaca aagtetaege etgegaagte 600
acccatcagg gcctgagyty gcccgtcaca aagagcttca acaggggaga gtgttaa
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<213> Artificial Sequence
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ctcacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
qaaaaaccag atcatttatt cactggtcta ataggtggta ccaataaccg ggctccgggt 180
gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactccaa cctctgggtr 300
ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcaccetga egetgageaa agcagaetae gagaaacaea aagtetaege etgegaagte 600
acccatcagg gcctgagyty gcccgtcaca aagagcttca acaggggaga gtgttaa
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<223> Description of Artificial Sequence: nucleic acid
      that encodes light chain mutant with Cys
      substituted for Ser at position 96 of CHA255
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ctcacttgtc gctcaagtat tggggctgtt acaactagta actatgccaa ctgggtccaa 120
gaaaaaccag atcatttatt cactggtcta ataggtggta ccaataaccg ggctccgggt 180
gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactgcaa cctctgggtr 300
ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
atcttcccqc catctqatqa qcaqttqaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
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ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

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Ser	Asn	Tyr 35	Ala	Asn	Trp	Val	Gln 40	Glu	Lys	Pro	Asp	His 45	Leu	Phe	Thr
Gly	Leu 50	Ile	Gly	Gly	Thr	Asn 55	Asn	Arg	Ala	Pro	Gly 60	Val	Pro	Ala	Arg
Phe 65	Ser	Gly	Ser	Leu	Ile 70	Gly	Asp	Lys	Ala	Ala 75	Leu	Thr	Ile	Thr	Gly 80
				85			Arg		90					95	
Cys	Leu	Trp	Val 100	Phe	Gly	Gly	Gly	Thr 105	Lys	Leu	Thr	Val	Leu 110	Ser	Arg
		115					Phe 120					125			
	130		_			135	Val		_		140				_
145				-	150		Trp	_		155					160
_				165			Thr		170					175	
-			180				Thr	185				_	190		
His	Lys	Val 195	Tyr	Ala	Cys	Glu	Val 200	Thr	His	Gln	Gly	Leu 205	Ser	Xaa	Pro
Val	Thr 210	Lys	Ser	Phe	Asn	Arg 215	Gly	Glu	Cys						

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      sequence of unmodified light chain of CHA255
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Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
                 85
Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                            120
        115
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
                        135
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                                         155
                    150
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                                     170
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
                                 185
                                                     190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
                            200
                                                 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 7
<211> 218 ·
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<213> Artificial Sequence
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<223> Description of Artificial Sequence:polypeptide
      sequence of mutant light chain with Cys
      substituted for Ser at position 96 of CHA255
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Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys
Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
                        135
    130
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                    150
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165
                                    170
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
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                                                 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210
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Gly	Gly	Phe	Leu 20	Lys	Leu	Ser	Cys	Ala 25	Ala	Ser	Gly	Phe	Thr 30	Leu	Ser
Gly	Glu	Thr 35	Met	Ser	Trp	Val	Arg 40	Gln	Thr	Pro	Glu	Lys 45	Arg	Leu	Glu
Trp	Val 50	Thr	Thr	Thr	Leu	Ser 55	Gly	Gly	Gly	Phe	Thr 60	Phe	Tyr	Ser	Ala
Ser 65	Val	Lys	Gly	Arg	Phe 70	Thr	Ile	Ser	Arg	Asp 75	Asn	Ala	Gln	Asn	Asn 80
Leu	Tyr	Leu	Gln	Leu 85	Asn	Ser	Leu	Arg	Ser 90	Glu	Asp	Thr	Ala	Leu 95	Tyr
Phe	Cys	Ala	Ser 100	His	Arg	Phe	Val	His 105	Trp	Gly	His	Gly	Thr 110	Leu	Val
Thr	Val	Ser 115	Ala	Ala	Lys	Thr	Thr 120	Gly	Pro	Ser	Val	Phe 125	Pro	Leu	Ala
Pro	Ser 130	Ser	Lys	Ser	Thr	Ser 135	Gly	Gly	Thr	Ala	Ala 140	Leu	Gly	Cys	Leu
Val 145	Lys	Asp	Tyr	Phe	Pro 150	Glu	Pro	Val	Thr	Val 155	Ser	Trp	Asn	Ser	Gly 160
Ala	Leu	Thr	Ser	Gly 165	Val	His	Thr	Phe	Pro 170	Ala	Val	Leu	Gln	Ser 175	Ser
Arg	Leu	Tyr	Phe 180	Leu	Ser	Ser	Val	Val 185	Thr	Val	Pro	Phe	Asn 190	Ser	Leu
Gly	Thr	Gln 195	Thr	Tyr	Ile	Cys	Asn 200	Val	Asn	His	Lys	Pro 205	Ser	Asn	Thr
Lys	Val 210	Asp	Lys	Lys	Ala	Glu 215	Pro	Lys	Ser	Cys	Asp 220	Lys	Ser	Arg	Gly
Pro 225	Phe	Glu	Gly	Lys	Pro 230	Ile	Pro	Asn	Pro	Leu 235	Leu	Gly	Leu	Asp	Ser 240
Thr	Arg	Thr	Gly	His 245	His	His	His	His	His 250						

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	Description of Artificial Sequence: T7 promoter	
12007	primer	
	primer	
400		
<400>		~ -
ctaata	acgac tcactatagg g	21
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	Artificial Sequence	
(213/	Artificial bequence	
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ctacac	ggtcg actctagagg atctactagt	30
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<213>	Artificial Sequence	
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12201		
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catgco	etgca ggtcgactct agaggatcta ctagt	33
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	Artificial Sequence	
(213)	Altilitial bequence	
<220>		
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ttctat	gete tatggtacag caacetetgg gtatteggt	39
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-270	12	
<210>		
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-223/	primer S95C	
	bramer 2000	
400	12	
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atacco	cagag gttgcagtac catagagcac	30

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<400	)> 14	Į.															
ggtt	ttcc	cca g	gtcad	cgaco	3											19	
<210	)> 15	5															
<211	.> 30	)															
	2 > DN																
			icial	l Sec	nuena	re.											
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<220	١~																
		ecri	intic	n 01	F Drt	ific	rial	Sem	ience	- · mıı t	ager	nesis	3				
<b>422</b> 3			. N96		LAL	-111	.141	Sequ	201100	a c	-ugui	1001	•				
	ρı	. I IIICI	LNJ	J.C.													
-400	)> 15	-															
							. ~ ~ ~ .	_								30	
acac	ccaç	gag g	gcago	ctgta	ac ca	acaga	agcac	ن								30	
		_															
	)> 16																
	.> 36																
	?> DI																
<213	3 > A1	rtifi	icial	l Sec	queno	ce											
<220	) >																
<223	> De	escri	iptic	on of	E Art	ific	cial	Sequ	ience	e:V-F	I sec	quenc	ce of	=			
	CF	IA255	5														
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<221	.> CI	s															
<222	!> (1	L)	(360)	)													
	•	•															
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			cta	ata	gag	tct	aaa	aaa	gac	tca	ata	aaq	cct	qqa	qqq	48	
									Asp								
1	vai	1111	пси	5	OIU	501	917	OI,	10	501		_1_		15	<b>U</b> -1		
_				J					10								
			a+ a	+	+~+	~~~	~~~	tat	gga	++0	act	++2	201	aat	ma a	96	
																70	
ser	Leu	гÀг		ser	Cys	Ата	Ala		Gly	Pne	1111	ьец		GIY	Giu		
			20					25					30				
																2 4 4	
									gag							144	
Thr	Met		Trp	Val	Arg	Gln		Pro	Glu	Lys	Arg		GIu	Trp	vaı		
		35					40					45					
									acc							192	
Ala	Thr	Thr	Leu	Ser	Gly	Gly	Gly	Phe	Thr	Phe	Tyr	Ser	Ala	Ser	Val		
	50				-	55	-				60						•
aaq	gat	cat	ttc	acc	atc	tcc	aga	gac	aat	gcc	cag	aac	aac	ctc	tat	240	
									Asn								
65	1	⊐			70		9			75					80		
05					, 0												

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cta caa ctg aat agt ctg agg tct gag gac acg gcc ttg tat ttc tgt Leu Gln Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Phe Cys 85 90 95	288										
gca agt cat cgg ttt gtt cac tgg ggc cac ggg act ctg gtc act gtc Ala Ser His Arg Phe Val His Trp Gly His Gly Thr Leu Val Thr Val 100 105 110	336										
tct gca gcc aaa acg aca ccc cca Ser Ala Ala Lys Thr Thr Pro Pro 115 120	360										
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Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Gly Glu 20 25 30											
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Ala Thr Thr Leu Ser Gly Gly Gly Phe Thr Phe Tyr Ser Ala Ser Val											
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Asn Leu Tyr 65 70 75 80											
Leu Gln Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Phe Cys 85 90 95											
Ala Ser His Arg Phe Val His Trp Gly His Gly Thr Leu Val Thr Val											
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<210> 18 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:cloning primer with XhoI site											
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<220>
<221> CDS
<222> (1)..(405)
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                                                                   48
Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr
gtc aca ctc act tgt cgc tca agt att ggg gct gtt aca act agt aac
                                                                   96
Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser Asn
tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggt cta
Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu
                             40
ata ggt ggt acc aat aac cgg gct ccg ggt gtt cct gcc aga ttc tca
Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe Ser
     50
ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca cag
Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln
65
                     70
                                                                   288
act gaa gat gag gca aga tat ttc tgt gct cta tgg tac tgc aac ctc
Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys Asn Leu
                                      90
tgg gtg ttc ggt gga gga acc aaa ctg act gtc cta agc cag ccc aag
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro Lys
            100
                                 105
                                                     110
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tct tcg cca tca gtc acc ctg ttt ccg ccc tcc tct gaa gag cta agc Ser Ser Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Ser 115 120 125	384
ttg gga atc gga ttc ccg ggn Leu Gly Ile Gly Phe Pro Gly 130 135	405
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Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr Ser Asn 20 25 30	
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Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe Ser 50 55 60	
Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln 65 70 75 80	
Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys Asn Leu 85 90 95	
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro Lys 100 105 110	
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ctcgcatgcg cttaggacag tcagttt
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